

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/596,784

TECH CENTER 1600

DATE: 11/01/2000
TIME: 03:02:30

INPUT SET: S36052.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Bogdanove, Adam J.
Kim, Jihyun Francis
Wei, Zhong-Min
Beer, Steven V.

(ii) TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM
ERWINIA AMYLOVORA, ITS USE, AND ENCODING GENE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
(B) STREET: P.O. Box 1051, Clinton Square
(C) CITY: Rochester
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 14603

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/596,784
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/120,663
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Goldman, Michael L.
(B) REGISTRATION NUMBER: 30,727
(C) REFERENCE/DOCKET NUMBER: 19603/1661

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (716) 263-1304
(B) TELEFAX: (716) 263-1600

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 5517 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: DNA (genomic)
57
58
59
60
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63 ATGGAATTAA AATCACTGGG AACTGAACAC AAGGCGGCAG TACACACAGC GGCGCACAAAC 60
64
65 CCTGTGGGGC ATGGTGTTC CTTACAGCAG GGCAGCAGCA GCAGCAGCCC GCAAAATGCC 120
66
67 GCTGCATCAT TGGCGGCAGA AGGCAAAAAT CGTGGGAAAA TGCCGAGAAT TCACCAGCCA 180
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69 TCTACTGCGG CTGATGGTAT CAGCGCTGCT CACCAGCAAA AGAAATCCTT CAGTCTCAGG 240
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71 GGCTGTTTGG GGACGAAAAA ATTTTCCAGA TCGGCACCGC AGGGCCAGCC AGGTACCACC 300
72
73 CACAGCAAAG GGGCAACATT GCGCGATCTG CTGGCGCGGG ACGACGGCGA AACGCAGCAT 360
74
75 GAGGCGGCCG CGCCAGATGC GGCGCGTTTG ACCCGTTCGG GCGGCGTCAA ACGCCGCAAT 420
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77 ATGGACGACA TGGCCGGGCG GCCAATGGTG AAAGGTGGCA GCGGCGAAGA TAAGGTACCA 480
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79 ACGCAGCAAA AACGGCATCA GCTGAACAAT TTTGGCCAGA TGCGCCAAAC GATGTTGAGC 540
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81 AAAATGGCTC ACCCGGCTTC AGCCAACGCC GGCGATCGCC TGCAGCATTC ACCGCCGCAC 600
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83 ATCCCGGGTA GCCACCACGA AATCAAGGAA GAACCGGTTG GCTCCACCAG CAAGGCAACA 660
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85 ACGGCCCACG CAGACAGAGT GGAAATCGCT CAGGAAGATG ACGACAGCGA ATTCCAGCAA 720
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87 CTGCATCAAC AGCGGCTGGC GCGCGAACGG GAAAATCCAC CGCAGCCGCC CAAACTCGGC 780
88
89 GTTGCCACAC CGATTAGCGC CAGGTTTCAG CCCAAACTGA CTGCGGTTGC GGAAAGCGTC 840
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91 CTTGAGGGGA CAGATACCAC GCAGTCACCC CTTAAGCCGC AATCAATGCT GAAAGGAAGT 900
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93 GGAGCCGGGG TAACGCCGCT GGCGGTAACG CTGGATAAAG GCAAGTTGCA GCTGGCACCG 960
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95 GATAATCCAC CCGCGCTCAA TACGTTGTTG AAGCAGACAT TGGGTAAAGA CACCCAGCAC 1020
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97 TATCTGGCGC ACCATGCCAG CAGCGACGGT AGCCAGCATC TGCTGCTGGA CAACAAAGGC 1080
98
99 CACCTGTTTG ATATCAAAAG CACCGCCACC AGCTATAGCG TGCTGCACAA CAGCCACCCC 1140

100								1200
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103	AGCGGCAAGA	TCTCGCTGGG	GAGCGGTACG	CAAAGTCACA	ACAAAACAAT	GCTAAGCCAA		
104								1320
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106								1380
107	CGGCCGCAGG	GCGAGTCAAT	CCGCCTGCAT	GACGACAAAA	TTCATATCCT	GCATCCGGAG		
108								1440
109	CTGGGCGTAT	GGCAATCTGC	GGATAAAGAT	ACCCACAGCC	AGCTGTCTCG	CCAGGCAGAC		
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111	GGTAAGCTCT	ATGCGCTGAA	AGACAACCGT	ACCCTGCAAA	ACCTCTCCGA	TAATAAATCC		
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113	TCAGAAAAGC	TGGTCGATAA	AATCAAATCG	TATTCCGTTG	ATCAGCGGGG	GCAGGTGGCG		
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124								1920
125	TCTGGATTTT	TCCATGACGA	CCACGGCCAG	CTTAATGCGC	TGGTGAAAAA	TAAC TTCAGG		
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127	CAGCAGCATG	CCTGCCCCGT	GGGTAACGAT	CATCAGTTTC	ACCCCGGCTG	GAACCTGACT		
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133	GACCAGCTGA	CCAAAGGGTG	GACTGGCGCG	GAGTCAGATT	GTAAGCAGCT	GAAAAAAGGC		
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135	CTGGATGGAG	CAGCTTATCT	ACTGAAAGAC	GGTGAAGTGA	AACGCCTGAA	TATTAATCAG		
136								2280
137	AGCACCTCCT	CTATCAAGCA	CGGAACGGAA	AACGTTTTTT	CGCTGCCGCA	TGTGCGCAAT		
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139	AAACCGGAGC	CGGGAGATGC	CCTGCAAGGG	CTGAATAAAG	ACGATAAGGC	CCAGGCCATG		
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141	GCGGTGATTG	GGGTAAATAA	ATACCTGGCG	CTGACGGAAA	AAGGGGACAT	TCGCTCCTTC		
142								2460
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145	ATCAGCGGCG	AACTGAAAGA	CATTCATGTC	GACCACAAGC	AGAACCTGTA	TGCCTTGACC		
146								2580
147	CACGAGGGAG	AGGTGTTTCA	TCAGCCGCGT	GAAGCCTGGC	AGAATGGTGC	CGAAAGCAGC		
148								2640
149	AGCTGGCACA	AACTGGCGTT	GCCACAGAGT	GAAAGTAAGC	TAAAAAGTCT	GGACATGAGC		
150								2700
151	CATGAGCACA	AACCGATTGC	CACCTTTGAA	GACGGTAGCC	AGCATCAGCT	GAAGGCTGGC		
152								

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153	GGCTGGCACG CCTATGCGGC ACCTGAACGC GGGCCGCTGG CGGTGGGTAC CAGCGGTTCA	2760
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156		
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158		
159	AGCAGTAAAT TTTCCGAAAG GATCCGCGCC TATGCGTTCA ACCCAACAAT GTCCACGCCG	2940
160		
161	CGACCGATTA AAAATGCTGC TTATGCCACA CAGCACGGCT GGCAGGGGCG TGAGGGGTTG	3000
162		
163	AAGCCGTTGT ACGAGATGCA GGGAGCGCTG ATTAAACAAC TGGATGCGCA TAACGTTCTG	3060
164		
165	CATAACGCGC CACAGCCAGA TTTGCAGAGC AAAGTGGAAA CTCTGGATTT AGGCGAACAT	3120
166		
167	GGCGCAGAAT TGCTTAACGA CATGAAGCGC TTCCGCGACG AACTGGAGCA GAGTGCAACC	3180
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169	CGTTCGGTGA CCGTTTTAGG TCAACATCAG GGAGTGCTAA AAAGCAACGG TGAAATCAAT	3240
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171	AGCGAATTTA AGCCATCGCC CGGCAAGGCG TTGGTCCAGA GCTTTAACGT CAATCGCTCT	3300
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173	GGTCAGGATC TAAGCAAGTC ACTGCAACAG GCAGTACATG CCACGCCGCC ATCCGCAGAG	3360
174		
175	AGTAAACTGC AATCCATGCT GGGGCACTTT GTCAGTGCCG GGGTGGATAT GAGTCATCAG	3420
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177	AAGGGCGAGA TCCCCTGGG CCGCCAGCGC GATCCGAATG ATAAAACCGC ACTGACCAAA	3480
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179	TCGCGTTTAA TTTTAGATAC CGTGACCATC GGTGAAGTGC ATGAAGTGGC CGATAAGGCG	3540
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181	AAACTGGTAT CTGACCATAA ACCCGATGCC GATCAGATAA AACAGCTGCG CCAGCAGTTC	3600
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183	GATACGCTGC GTGAAAAGCG GTATGAGAGC AATCCGGTGA AGCATTACAC CGATATGGGC	3660
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185	TTCACCCATA ATAAGGCGCT GGAAGCAAAC TATGATGCGG TCAAAGCCTT TATCAATGCC	3720
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187	TTTAAGAAAG AGCACCACGG CGTCAATCTG ACCACGCGTA CCGTACTGGA ATCACAGGGC	3780
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191	ATGAGCTTCA GCCGGTCATA TGGCGGGGCG GTCAGCACTG TCTTTGTGCC TACCCTTAGC	3900
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193	AAGAAGGTGC CAGTTCCGGT GATCCCCGGA GCCGGCATCA CGCTGGATCG CGCCTATAAC	3960
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195	CTGAGCTTCA GTCGTACCAG CGGCGGATTG AACGTCAGTT TTGGCCGCGA CGGCGGGGTG	4020
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197	AGTGGTAAAC TCATGGTCGC TACCGGCCAT GATGTGATGC CCTATATGAC CGGTAAGAAA	4080
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199	ACCAGTGCAG GTAACGCCAG TGAAGGTTG AGCGCAAAAC ATAAATCAG CCCGGACTTG	4140
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201	CGTATCGGCG CTGCTGTGAG TGGCACCCTG CAAGGAACGC TACAAAACAG CCTGAAGTTT	4200
202		
203	AAGCTGACAG AGGATGAGCT GCCTGGCTTT ATCCATGGCT TGACGCATGG CACGTTGACC	4260
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206	TTTAGCGTCG	ATACCTCGGC	AAATCTGGAT	CTGCGTGCCG	GTATCAATCT	GAACGAAGAC	4380
207	GGCAGTAAAC	CAAATGGTGT	CACTGCCCCG	GTTTCTGCCG	GGCTAAGTGC	ATCGGCAAAC	4440
208	CTGGCCGCCG	GCTCGCGTGA	ACGCAGCACC	ACCTCTGGCC	AGTTTGGCAG	CACGACTTCG	4500
209	GCCAGCAATA	ACCGCCCAAC	CTTCCTCAAC	GGGGTCGGCG	CGGGTGCTAA	CCTGACGGCT	4560
210	GCTTTAGGGG	TTGCCCATTG	ATCTACGCAT	GAAGGGAAAC	CGGTCTGGGAT	CTTCCCGGCA	4620
211	TTTACCTCGA	CCAATGTTTC	GGCAGCGCTG	GCGCTGGATA	ACCGTACCTC	ACAGAGTATC	4680
212	AGCCTGGAAT	TGAAGCGCGC	GGAGCCGGTG	ACCAGCAACG	ATATCAGCGA	GTTGACCTCC	4740
213	ACGCTGGGAA	AACACTTTAA	GGATAGCGCC	ACAACGAAGA	TGCTTGCCGC	TCTCAAAGAG	4800
214	TTAGATGACG	CTAAGCCCGC	TGAACAACTG	CATATTTTAC	AGCAGCATTT	CAGTGCAAAA	4860
215	GATGTCGTCG	GTGATGAACG	CTACGAGGCG	GTGCGCAACC	TGAAAAAACT	GGTGATACGT	4920
216	CAACAGGCTG	CGGACAGCCA	CAGCATGGAA	TTAGGATCTG	CCAGTCACAG	CACGACCTAC	4980
217	AATAATCTGT	CGAGAATAAA	TAATGACGGC	ATTGTGAGC	TGCTACACAA	ACATTTTCGAT	5040
218	GCGGCATTAC	CAGCAAGCAG	TGCCAAACGT	CTTGGTGAAA	TGATGAATAA	CGATCCGGCA	5100
219	CTGAAAGATA	TTATTAAGCA	GCTGCAAAGT	ACGCCGTTCA	GCAGCGCCAG	CGTGTCGATG	5160
220	GAGCTGAAAG	ATGGTCTGCG	TGAGCAGACG	GAAAAAGCAA	TACTGGACGG	TAAGGTCGGT	5220
221	CGTGAAGAAG	TGGGAGTACT	TTTCCAGGAT	CGTAACAACT	TGCGTGTTAA	ATCGGTCAGC	5280
222	GTCAGTCAGT	CCGTCAGCAA	AAGCGAAGGC	TTCAATACCC	CAGCGCTGTT	ACTGGGGACG	5340
223	AGCAACAGCG	CTGCTATGAG	CATGGAGCGC	AACATCGGAA	CCATTAATTT	TAAATACGGC	5400
224	CAGGATCAGA	ACACCCACG	GCGATTTACC	CTGGAGGGTG	GAATAGCTCA	GGCTAATCCG	5460
225	CAGGTCGCAT	CTGCGCTTAC	TGATTTGAAG	AAGGAAGGGC	TGGAAATGAA	GAGCTAA	5517

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1838 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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SEQUENCE VERIFICATION REPORT
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Original Text

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SEQUENCE MISSING ITEM REPORT
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SEQUENCE CORRECTION REPORT
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